03004.5 Page 1 of 7

12-4-01 #45

12-4-61 AD

OIPE

RAW SEQUENCE LISTING DATE: 12/04/2001 PATENT APPLICATION: US/09/855,612A TIME: 17:55:19

```
1 <110> APPLICANT: SPIES, THOMAS
        SPIES, VERONIKA
 3 <120> TITLE OF INVENTION: CELL STRESS REGULATED HUMAN MHC CLASS I GENE
 4 <130> FILE REFERENCE: FHCC:003WO
 5 <140> CURRENT APPLICATION NUMBER: 09/855,612A
 6 <141> CURRENT FILING DATE: 2001-05-14
 7 <150> PRIOR APPLICATION NUMBER: US/09/303,161
 8 <151> PRIOR FILING DATE: 1999-04-29
                                                          ENTERED
 9 <150> PRIOR APPLICATION NUMBER: PCT/US97/29179
10 <151> PRIOR FILING DATE: 1997-10-29
11 <150> PRIOR APPLICATION NUMBER: USAN60/029,044
12 <151> PRIOR FILING DATE: 1996-10-29
13 <160> NUMBER OF SEQ ID NOS: 16
14 <170> SOFTWARE: PatentIn Ver. 2.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 11722
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo Sapiens
20 <400> SEQUENCE: 1
         cactgettga geogetgaga gggtggegae gteggggeea tggggetggg eeeggtette 60
21
22
         ctqcttctqq ctqqcatctt cccttttqca cctccqqqaq ctqctqctqq tqaqtqqcqt 120
         tectggeggt ceteggegga gegggageag tgggaegttt eegggggteg ggtgggtage 180
23
         ggcgagcgct gtgcggtcag ggcggggctc ctgtgccctg tcggtggcgc agggagctgg 240
24
         acgoggooog ttacogocac acttoagoco tgottocoog toacttttoa gtootootog 300
25
         ggategegea teacetgeae tttetggtet eeteetgete ttteteteet egegteteet 360
26
27
         ccgcttcctc tcacttttcg gacaaaccag tccttctgag gcccatgggt tcccgggctg 420
         ceteegggge tgeteetgtg aatggeatte gagtgeeett eeagegegge caetgaagea 480
28
29
         qccacaacce coggtgetog gggcggetot caggteeotg aagteetgte etetocogga 540
30
         geegaegtgt teteagetee tgggeegeag eteetggagt aggggeeete ettteteggg 600
31
         acceggaget ggtgetteet getgetgtgg ggaetgtggg gggteetgae teteaagetg 660
         aggggttgga gtetgeagge teegggeaga ggattettee tgegaettet eteateeeea 720
32
33
         geteattete ecctegeete tggeteegag ggteetetee teteteteat eccaeceeta 780
         ctaatgacca gtgatctaag gacaccagat teceteteae etecteeetg cecateteag 840
34
35
         ggcccgctga gtccttttgc cctcccagct ccctgctacc ccttcctgtg tgctgttctc 900
36
         tgatecattt ctagggtgte etetgeeete ateceetgte eeegeeaceg aagteeetee 960
37
         tgcacccctt atgggccttt cctacaagca gccttcaccc agtgctgccc ctatgcctcc 1020
38
         ccqttcccaa atqtccctqa ctctaacttt ctqqtqctqc cttttatccq ggggggtctt 1080
39
         ccctccatcc cactcccctc cagaccccca aggggaaccc tgatgctaat ggcagttggg 1140
40
         cettaggeag ggegeaggge agegeagatg ecceeteece tecagtgeag atgeetgtte 1200
41
         tggaccetge etcattgtgg eccetteece acteetteat ceteageete accetettga 1260
42
         ggaccccacc ctccagccca caggtgctgg accatccctc cctggtccct ccgccctct 1320
43
         ccaccttggg accttgtgct gctcctatct cttgcccage tgccttgggc cctcagcacg 1380
         ttctcatctt tcagtgggaa agtgggagtg ctggagcata tgacagtgct gagcatcttt 1440
44
45
         eccaageece acceteece agageaceet ecceteetgt ceteaceeta ecceaagete 1500
46
         teceaeagte aetectgeee catgeteatg eegeceteea gttettgete tgeeeatete 1560
47
         ccctccccaa cccagaccta aaacaggctg ttgggccaac tgttccttga ccttccttct 1620
48
         tttcttttgg ttccttgacc ccagtgggct ctcactcccc acaccgcata tctaaaatct 1680
```



Input Set : N:\Crf3\RULE60\09855612A.RAW
Output Set: N:\CRF3\12042001\1855612A.raw

49 gttttgcctg ctcttggggt gccactgctc cccctccagc attactcctt ttggcaggtc 1740 50 cttcctcagg ctgagaatct ccccctctac cttggttttc tctctctggc cagcaccccc 1800 actccttqct ttgtttttaa tttttaactt ttgtttgggt acgtagtaga tatatatgta 1860 51 52 tatatttatg gggtacatgg gatattttga cacaggccta caatatgtaa taatcacatc 1920 53 agggtaaatg ggttatatca caacaagcat ttatcctttc tttgtgctac aaacaatccc 1980 attatgctct ttcagttatt tttaaatgta caataaatta ttgttgactg tactcaccct 2040 54 gctgtgctat ctactagatc ttattcattc taattatatt tttgtaccca ttattaacca 2100 55 tecetgetee eccaeteece actaecette teageetetg gtaateatea ttetattgte 2160 56 57 tetececatg aggtecattg ttttaaattt tggetgeeac aaataagtga gaacatgeaa 2220 agtttgtctg tctgggcctg gggcttattt cacttcacag gatgacctcc agttctttgc 2280 58 59 aaatgacacg atggetgaat agtteteeac atacacatgt acaccacatt ttetttatee 2340 atgcgtctgt tgatggacac ttagattgct tgcagatctt ggctactttg aatagtgctg 2400 60 caataaacat ggaaaagtag atagctcttt aatataccga tttcctttct ttggagtata 2460 61 tgcctaacag tgggagtgct ggagcatatg acagctctat tgtattttta gtttttggaa 2520 62 quacetecae attqttteee ataqtqqttq tactaqttta egtteecaee aacaqtqtae 2580 63 atcctcacca gcattcctta tttctacatc ctcqccagca ttccttattq cctqtcttct 2640 64 ggataaaagc cagtttatct ggggtgggat gttatctcgt aggagttttg atttgccttc 2700 65 66 atctgttgac gaatgatgtt gagcaccttt tcatatacct gtttgccatt tatatgtctt 2760 67 cttttgagaa atgactattc agatcttttc tcatttttaa attggattat tatatttttt 2820 68 ttcctatagt tgttcgagct ccttatatgt ttcagttact gatcctttgt cagatgaata 2880 69 gtttgaaaat attttctccc attcttggat ggtctcttca ttttgtttat tgtttccttt 2940 70 gctgtgcaga agccttttta cttgatatga tcccatttat gcaattttac tttggttacc 3000 71 tgtgcttgtg gggtattact ttaaaaatct ttgcccagtc caatatccta gagagtttcc 3060 ccaatgtttt cttgtatagt ttcatagttt gaggtcatag atttacatct ttaatccact 3120 72 73 ttgatttgat ttttgtatat ggtgaaagac agggtctagt ttcattcttc tgcataagga 3180 74 tatctagttt ccccagcacc atttttgaag agactctcct ttgccaatgt gtgttcttgg 3240 75 tacctttgtt ggaaatgagt ttactgtaga tgtatggaat tgtttctggg ttctctattc 3300 76 tgtttcattg gtctgtgtgt ctgtttttat gccagtatca tgctgttttg gttactgtag 3360 77 ctctgtagta taatttgaag tcagataatg tgattcctct agttttgttc attttgctca 3420 78 ggatagettt atetattetg gtttttttgt ggtteeatat geattttagg attattttta 3480 79 ttatttctgt gaagaatgtc attagtgttt tgatagggat tgcattgaat ctgtagatta 3540 80 ctttgggtag tatggatatt tcaacaaaac tgattcttcc aatccatgaa cgtggactat 3600 81 cttttccatt ttttgtgtcc ttcaattttt tgcatcagtg ttttttgttt ttggtttttg 3660 82 agatggagtt tcactcttgt tgcccaggct agaatgcaag ggtgtgatct tggctcaccg 3720 83 caaceteege eteceaggtt caagetatte ttetgeetea geeteecaag tagetgggat 3780 tacaggcatg tgccactgtg cctggctaat tttctatttt tattagagat ggggtttctc 3840 84 85 tatgttggcc aggctagtct tgaactcctg acctcaggtg atccacctgc ctcggcctcc 3900 86 caaagtgctg ggattacagg catgagccac cacgcccagc cacatcactg ttttatagtt 3960 87 88 tgtagctatt gtaaatggga ttcgtttctt gatttctttt tcagattatt tgctgttagc 4080 89 actgattttt gcatgttgat tttgtatcct gcaactttac tgaatttgtt cttcagttct 4140 90 aatggttttt tggtggagte tttaggtttt tecaaatate agaccacatg atetgcaaac 4200 aaggataatt tgacttette tttteeagtt ttaatgeeet ttetttettt eteetgtetg 4260 91 92 attgctctag ttaggatctg cagtactgtg ttgcataact gtggtaaaat tagtcatcct 4320 93 tgtcttattc cagatcttag agaaaaggct ttcagttttc ccccattcag tatgttacta 4380 94 gctgtgagtt tqtcatatat ggcttttatt atattgaggt ctqttccttg tatacttagt 4440 95 tttttgagag tttttatcat gaagggatgt tgaatttatc aaatgctttt tcagtatcaa 4500 96 ttgaatgata ctggcttttg tcctttattc tgttgatatg acgtattaca ttgattgatt 4560 97 tgtgtatgtt aaatcatcct tgcatacctg gaatacattc cacttgctca taaagaatga 4620



Input Set: N:\Crf3\RULE60\09855612A.RAW
Output Set: N:\CRF3\12042001\1855612A.raw

98 tettttttaa tgtattgttg aatgtggttt getagtattt eettgaegat ttttgeateg 4680 99 gtgttcatca gggatatagg cctgtagttt tcttttttat gatgtgtctt tgcctggttt 4740 100 ttgtatcagg atattcctgg ctttgtaaaa tgagtttgga agtattccct cctcctctat 4800 ttttcagaac agtttgaata ggactgacat atgttgttct ttaaaagttt aattgtggta 4860 101 102 aattatacat tacataaatt ttactqtttt aaccactttt aaqtqtatac tcqqtqqcat 4920 103 tagatacatt cacatttttg tgcaacccaa aactctgtgc ccattaatcg gtaactcccc 4980 104 attecteect acctetggee cetggtaace accattetae tttttgttte tatgaatttg 5040 105 accactctag gtacctcatt taagcagaat catgtaatgt ttgtcttttt gtttctggct 5100 tatttcactt ataatatttt tgaggttcgg tgggcacagt ggctcacgcc tggatttcca 5160 106 107 gcactttggg aggctgaagc aggtggatca cctgagtttc ggagttcgaa accagcctgg 5220 ccaacatggt gaaaccccat ctctactaaa aataataaaa gttagccggg cgtgatggcg 5280 108 109 ggtgcctgta atcccaacta cttgggaggc tgaggcagga gaatcgcttg aatccgggaa 5340 110 gtggaggttg cagtgagctg agatcaggcc actgcactcc agcctgggca acaagagtga 5400 aattccatct ccaaaaaaaa aaaataaaac aataataata ataatatttt tgaggttcat 5460 111 112 ccaagttgta gtatgggtca gaatttcatt ccttttaagg atggataata ctcattatat 5520 gtatgtacca catcttggtt atccatcct cagacaatgg acacttgggt tacttctacc 5580 113 ttttggatat tggcaaatat ttcatttcct ttgggtatat atttatttcc tttgggtatt 5640 114 tettttgggt atatateeag aaatagaage agtacaeagg ggetteattt tetetgtete 5700 115 tttqccaacc ttqctctqtq tqtqtqta tqtqtqtqtq taqqtqtqtq ataacaqcca 5760 116 tectgattgg tttcaggtgg cateteattg tggtttggat ttgcatttte etaatgagtg 5820 117 ctgatattga gcatcttttc atgtgtttgt tgatcatttg taattttctt tgaagaattg 5880 118 119 qccatttaaq tettttqccc attttttccc ccacataqct tetettatca qatatatqac 5940 ttgcaatatt tatttcattt cggggttgat tgctttttca ctctgattgt gccctttgat 6000 120 121 gcatagatgt titgaatitt catcagteta cittgtcagt tetitetatt etatetgtge 6060 tttggtgtca tatccatgaa agcactgtca aatcctatgt catgaacatt atccccaatg 6120 122 123 tttgcttcta agaaattttt aggttttagt tcttgagtgt agagtttagg tctttgattc 6180 124 attttgagtt aatttttgta tatagtgcaa attaagggtc caattttatt ttaacacccc 6240 125 ctgcccccag aactatttgc tgaaaagatc aactgactct ttgtcacctg ctcaccccag 6300 126 tggacactag ctgttccatc caattgctgt cctggggcct tgtcatgcta ctcttccact 6360 127 ttgaacccaa gcccacaccg ttcgttgctc ccctctggga tactgacccc actataaact 6420 128 tetetgggge tacaacette etaccetttg tgeeteatga ceaececete cettgteece 6480 129 qccatqccca tqatqaqtct cttctcqaqq caqctcccct tqcctccatc tcaccctcaq 6540 130 cctatgcacc acagccacac tggacatggg tccctctgag cctgagtccc ttcccattcc 6600 131 caccatetee tetggeaaga cetteettee accacettea tgeteeteee ttgeeeetge 6660 agggeageet eteceettgg eccetattee ettaggggge ttgtggeeae ecagteettg 6720 132 133 cacctggcct acaagtttgc catcttcatt ccccttctt ctgttcatca gccccctcct 6780 134 ctatectece acceteacag tittetitgt atatgaaate etegtietig teeetitgee 6840 135 cqtqtqcatt tcctqcccca qqaaggttqq qacaqcaqac ctqtqtqtta aacatcaatq 6900 136 tqaaqttact tccaqqaaqa aqtttcacct qtqatttcct cttccccaqa qccccacaqt 6960 137 cttcgttata acctcacggt gctgtcctgg gatggatctg tgcagtcagg gtttcttgct 7020 138 gaggtacatc tggatggtca gcccttcctg cgctatgaca ggcagaaatg cagggcaaag 7080 139 ccccagggac agtgggcaga agatgtcctg ggaaataaga catgggacag agagaccagg 7140 140 gacttgacag ggaacggaaa ggacctcagg atgaccctgg ctcatatcaa ggaccagaaa 7200 141 gaaggtgaga gtcggcaggg gcaagagtga ctggagaggc cttttccaga aaagttaggg 7260 142 gcagagagca gggacctgtc tcttcccact ggatctggct caggctgggg gtgaggaatg 7320 143 ggggtcagtg gaactcagca gggaggtgag ccggcactca gcccacacag ggaggcatgg 7380 144 gggagggcca gggaggcgta ccccctgggc tgagttcctc acttgggtgg aaaggtgatg 7440 145 ggttcgggaa tggagaagtc actgctgggt gggggcaggc ttgcattccc tccaggagat 7500 146 tagggtctgt gagatccatg aagacaacag caccaggagc tcccagcatt tctactacga 7560



147				_		cccagtcctc	
148	cagageteag	accttggcca	tgaacgtcag	gaatttcttg	aaggaagatg	ccatgaagac	7680
149	_	_				gatatctaga	
150						cctctccctc	
151	caattctgct	agagttgcct	cacctccaag	atgtgtccag	ggaaaccctc	cctgtgctat	7860
152	ggatgaaggc	atttcctgtt	ggcacatcgt	gtcctgattt	tcctctattg	ttagagccac	7920
153	tggataaaga	cagtgggtca	gggactggac	catccagtgt	tgtaatcagg	gcaagtagag	7980
154	gaccctccga	cagaatcctg	agcctgtggt	gggtgtcagg	caggagagga	agccttcagg	8040
155	gccagggctg	cccctctgc	ctcccagcct	gcccatcctg	gagagttccc	tcctggcccc	8100
156	acaacccagg	agtccacccc	tgacatcccc	ctcctcagca	tcaatgtggg	gatcccagag	8160
157	cctgaggcca	cagtcccaag	gcccatcctc	ctgccagcct	ggaagaactg	ggccccagag	8220
158	tgaggacaga	cttgcaggtc	aggggtcccg	gagggcttca	gccagagtga	gaacagtgaa	8280
159	gagaaacagc	cctgttcctc	tcccctcctt	agaggggagc	agggcttcac	tggctctgcc	8340
160	ctttcttctc	cagtgccccc	catggtgaat	gtcacccgca	gcgaggcctc	agagggcaac	8400
161	atcaccgtga	catgcagggc	ttccagcttc	tatccccgga	atatcacact	gacctggcgt	8460
162	caggatgggg	tatctttgag	ccacgacacc	cagcagtggg	gggatgtcct	gcctgatggg	8520
163						gcagaggttc	
164						tggtgagcct	
165						gtggctctct	
166						gagtcattgg	
167						tattattatt	
168	_				_	tgagaaaagc	
169						cattgctcct	
170						tggggaattt	
171						agcgagggtc	
172						ggagggctgc	
173						ggcgcatcca	
174						acggcctcag	
175						agaggaatct	
176						tttctccagc	
177						ctgcctgtgt	
178						atctctgtcc	
179						tgtcctctgc	
180						gtttcttgca	
181						ggggcccagc	
182						ttcttctcca	
183						gtgctctgtg	
184						gcctggtaag	
185						atgggggatg	
186						ggcgacagta	
187						ctcatccttg	
188						tttgtccct	
189						gcaggtctgt	
190						ctggttccct	
191						gagtatgaag	
192						aagatattcg	
193						tattatatga	
193						cataatttca	
194						aacaggaact	
133	goldlycaal	cccaacayya	LLLUULaala	ctytaaayda	caccaacya	aacayyaact	T0200

196	caaattt	gga g	gece	cctct	c ca	agga	ggtt	c tgi	tgtg	gaga	tggt	tggct	tgt	ggcag	gtggca	10560
197	gttccca	ggt g	gcaga	agggt	g g	gcaga	aggc	a gc	ctca	ggct	aag	gggt	ctc	cccta	actcca	10620
198	catggag	aaa a	atcco	cttgt	a g	gttg	caage	g gca	agtg	geeg	ggt	ggaat	tcc	ctgct	taggga	10680
199	cagagca	gga a	aggco	ctcgc	ca go	cctca	accaa	a gca	agcag	gece	tggg	ggtg	gag	ctgc	gtttcc	10740
200	agggtta	age g	ggaco	caggo	ca go	gagta	agcg	g tta	actca	aaga	gcag	ggtca	aca	ggcti	tgggtt	10800
201	gtgaggg	tca g	ggaga	aggco	ca go	gcct	cctc	g ago	caag	gtgg	gggt	tccca	agg	gtcag	ggtcag	10860
202	gtgcaga	taa t	gtgg	gcago	cc a	egte	tttc	ate	gctg	ggcc	tgct	tgggd	ccc	ccca	ggcttc	10920
203	ctgatgg	ggt d	ccca	agtta	ag ga	agct	gcct	g cto	cagg	gctg	ggag	gggg	agg	agcad	ctgage	10980
204	tgcagata	aga g	gggca	agago	ec ca	acagi	tggg	age	ggcci	tgcc	ctg	gtgt	gta	ggtg	cctctg	11040
205	caggaga															
206	tcactgt															
207	tccttta	gtc t	tggg	ggcco	et ti	tecet	tacat	t gca	acgai	tgag	tggt	tgggd	cac	aggg	cacggg	11220
208	ctgatgt															
209	aagaaaa															
210	ctgaaga	_						_	-							
211	catttcc		_	-	-					_		_		-		
212	gacgagt				-			-	-			-				
213	gtccact	_	_		_		_		-	_		_	_	_		
214	ctgcctg															
215	gagaaaa			_							_		-		-	
216	gcatttg						, 5	5 .	J J J			,				11722
218 <210>	-	-		,		_										
219 <211>			_													
220 <212>																•
221 <213>	ORGANTSI	vr • Hc	omo s	Sapie	ns											
221 <213>			omo S	Sapie	ens											
222 <400>	SEQUENC	E: 2		-		Phe	Len	Len	Leu	Ala	Glv	Tle	Phe	Pro	Phe	
222 <400> 223	SEQUENCE Met Gly	E: 2		Pro		Phe	Leu	Leu		Ala	Gly	Ile	Phe		Phe	
222 <400> 223 224	SEQUENCE Met Gly	E: 2 Leu	Gly	Pro 5	Val				10		_			15		
222 <400> 223 224 225	SEQUENCE Met Gly	E: 2 Leu	Gly Gly	Pro 5	Val			Pro	10		_		Tyr	15		
222 <400> 223 224 225 226	SEQUENCE Met Gly 1 Ala Pro	E: 2 Leu Pro	Gly Gly 20	Pro 5 Ala	Val Ala	Ala	Glu	Pro 25	10 His	Ser	Leu	Arg	Tyr 30	15 Asn	Leu	
222 <400> 223 224 225 226 227	SEQUENCE Met Gly	E: 2 Leu Pro Leu	Gly Gly 20	Pro 5 Ala	Val Ala	Ala	Glu Ser	Pro 25	10 His	Ser	Leu	Arg Phe	Tyr 30	15 Asn	Leu	
222 <400> 223 224 225 226 227 228	Met Gly 1 Ala Pro Thr Val	E: 2 Leu Pro Leu 35	Gly Gly 20 Ser	Pro 5 Ala Trp	Val Ala Asp	Ala Gly	Glu Ser 40	Pro 25 Val	10 His Gln	Ser Ser	Leu Gly	Arg Phe 45	Tyr 30 Leu	15 Asn Ala	Leu Glu	
222 <400> 223 224 225 226 227 228 229	Met Gly 1 Ala Pro Thr Val Val His	E: 2 Leu Pro Leu 35	Gly Gly 20 Ser	Pro 5 Ala Trp	Val Ala Asp	Ala Gly Pro	Glu Ser 40	Pro 25 Val	10 His Gln	Ser Ser	Leu Gly Asp	Arg Phe 45	Tyr 30 Leu	15 Asn Ala	Leu Glu	
222 <400> 223 224 225 226 227 228 229 230	Met Gly 1 Ala Pro Thr Val Val His 50	E: 2 Leu Pro Leu 35 Leu	Gly Gly 20 Ser Asp	Pro 5 Ala Trp	Val Ala Asp Gln	Ala Gly Pro 55	Glu Ser 40 Phe	Pro 25 Val Leu	10 His Gln Arg	Ser Ser Tyr	Leu Gly Asp 60	Arg Phe 45 Arg	Tyr 30 Leu Gln	15 Asn Ala Lys	Leu Glu Cys	
222 <400> 223 224 225 226 227 228 229 230 231	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala	E: 2 Leu Pro Leu 35 Leu	Gly Gly 20 Ser Asp	Pro 5 Ala Trp	Val Ala Asp Gln	Ala Gly Pro 55	Glu Ser 40 Phe	Pro 25 Val Leu	10 His Gln Arg	Ser Ser Tyr Asp	Leu Gly Asp 60	Arg Phe 45 Arg	Tyr 30 Leu Gln	15 Asn Ala Lys	Leu Glu Cys Lys	
222 <400> 223 224 225 226 227 228 229 230 231 232	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala 65	E: 2 Leu Pro Leu 35 Leu	Gly Gly 20 Ser Asp	Pro 5 Ala Trp Gly	Val Ala Asp Gln Gly 70	Ala Gly Pro 55 Gln	Glu Ser 40 Phe Trp	Pro 25 Val Leu Ala	10 His Gln Arg	Ser Ser Tyr Asp	Leu Gly Asp 60 Val	Arg Phe 45 Arg	Tyr 30 Leu Gln	15 Asn Ala Lys Asn	Leu Glu Cys Lys 80	
222 <400> 223 224 225 226 227 228 229 230 231 232 233	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala	E: 2 Leu Pro Leu 35 Leu	Gly Gly 20 Ser Asp	Pro 5 Ala Trp Gly Gln	Val Ala Asp Gln Gly 70	Ala Gly Pro 55 Gln	Glu Ser 40 Phe Trp	Pro 25 Val Leu Ala	10 His Gln Arg Glu Thr	Ser Ser Tyr Asp	Leu Gly Asp 60 Val	Arg Phe 45 Arg	Tyr 30 Leu Gln	15 Asn Ala Lys Asn	Leu Glu Cys Lys 80	
222 <400> 223 224 225 226 227 228 229 230 231 232 233 234	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala 65 Thr Trp	E: 2 Leu Pro Leu 35 Leu Lys Asp	Gly 20 Ser Asp Pro	Pro 5 Ala Trp Gly Gln Glu 85	Val Ala Asp Gln Gly 70 Thr	Ala Gly Pro 55 Gln Arg	Glu Ser 40 Phe Trp Asp	Pro 25 Val Leu Ala	10 His Gln Arg Glu Thr	Ser Ser Tyr Asp 75 Gly	Leu Gly Asp 60 Val	Arg Phe 45 Arg Leu Gly	Tyr 30 Leu Gln Gly	15 Asn Ala Lys Asn Asp 95	Leu Glu Cys Lys 80 Leu	
222 <400> 223 224 225 226 227 228 229 230 231 232 233 234 235	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala 65	E: 2 Leu Pro Leu 35 Leu Lys Asp	Gly 20 Ser Asp Pro Arg Leu	Pro 5 Ala Trp Gly Gln Glu 85	Val Ala Asp Gln Gly 70 Thr	Ala Gly Pro 55 Gln Arg	Glu Ser 40 Phe Trp Asp	Pro 25 Val Leu Ala Leu Asp	10 His Gln Arg Glu Thr	Ser Ser Tyr Asp 75 Gly	Leu Gly Asp 60 Val	Arg Phe 45 Arg Leu Gly	Tyr 30 Leu Gln Gly Lys	15 Asn Ala Lys Asn Asp 95 His	Leu Glu Cys Lys 80 Leu	
222 <400> 223 224 225 226 227 228 229 230 231 232 233 234 235 236	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala 65 Thr Trp Arg Met	E: 2 Leu Pro Leu 35 Leu Lys Asp	Gly 20 Ser Asp Pro Arg Leu 100	Pro 5 Ala Trp Gly Gln Glu 85 Ala	Val Ala Asp Gln Gly 70 Thr	Ala Gly Pro 55 Gln Arg	Glu Ser 40 Phe Trp Asp	Pro 25 Val Leu Ala Leu Asp 105	10 His Gln Arg Glu Thr 90 Gln	Ser Ser Tyr Asp 75 Gly Lys	Leu Gly Asp 60 Val Asn Glu	Arg Phe 45 Arg Leu Gly	Tyr 30 Leu Gln Gly Lys Leu 110	15 Asn Ala Lys Asn Asp 95 His	Leu Glu Cys Lys 80 Leu Ser	
222 <400> 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala 65 Thr Trp	E: 2 Leu Pro Leu 35 Leu Lys Asp Thr	Gly 20 Ser Asp Pro Arg Leu 100	Pro 5 Ala Trp Gly Gln Glu 85 Ala	Val Ala Asp Gln Gly 70 Thr	Ala Gly Pro 55 Gln Arg	Glu Ser 40 Phe Trp Asp Lys Glu	Pro 25 Val Leu Ala Leu Asp 105	10 His Gln Arg Glu Thr 90 Gln	Ser Ser Tyr Asp 75 Gly Lys	Leu Gly Asp 60 Val Asn Glu	Arg Phe 45 Arg Leu Gly Gly Asn	Tyr 30 Leu Gln Gly Lys Leu 110	15 Asn Ala Lys Asn Asp 95 His	Leu Glu Cys Lys 80 Leu Ser	
222 <400> 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala 65 Thr Trp Arg Met Leu Gln	E: 2 Leu Pro Leu 35 Leu Lys Asp Thr	Gly 20 Ser Asp Pro Arg Leu 100 Ile	Pro 5 Ala Trp Gly Gln Glu 85 Ala Arg	Val Ala Asp Gln Gly 70 Thr His	Ala Gly Pro 55 Gln Arg Ile Cys	Glu Ser 40 Phe Trp Asp Lys Glu 120	Pro 25 Val Leu Ala Leu Asp 105 Ile	10 His Gln Arg Glu Thr 90 Gln	Ser Ser Tyr Asp 75 Gly Lys Glu	Leu Gly Asp 60 Val Asn Glu Asp	Arg Phe 45 Arg Leu Gly Gly Asn 125	Tyr 30 Leu Gln Gly Lys Leu 110 Ser	15 Asn Ala Lys Asn Asp 95 His	Leu Glu Cys Lys 80 Leu Ser	
222 <400> 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala 65 Thr Trp Arg Met Leu Gln Ser Ser	E: 2 Leu Pro Leu 35 Leu Lys Asp Thr	Gly 20 Ser Asp Pro Arg Leu 100 Ile	Pro 5 Ala Trp Gly Gln Glu 85 Ala Arg	Val Ala Asp Gln Gly 70 Thr His	Ala Gly Pro 55 Gln Arg Ile Cys	Glu Ser 40 Phe Trp Asp Lys Glu 120	Pro 25 Val Leu Ala Leu Asp 105 Ile	10 His Gln Arg Glu Thr 90 Gln	Ser Ser Tyr Asp 75 Gly Lys Glu	Leu Gly Asp 60 Val Asn Glu Asp Phe	Arg Phe 45 Arg Leu Gly Gly Asn 125	Tyr 30 Leu Gln Gly Lys Leu 110 Ser	15 Asn Ala Lys Asn Asp 95 His	Leu Glu Cys Lys 80 Leu Ser	
222 <400> 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala 65 Thr Trp Arg Met Leu Gln Ser Ser 130	E: 2 Leu Pro Leu 35 Leu Lys Asp Thr Glu 115 Gln	Gly 20 Ser Asp Pro Arg Leu 100 Ile	Pro 5 Ala Trp Gly Gln Glu 85 Ala Arg	Val Ala Asp Gln Gly 70 Thr His Val	Ala Gly Pro 55 Gln Arg Ile Cys Tyr 135	Glu Ser 40 Phe Trp Asp Lys Glu 120 Asp	Pro 25 Val Leu Ala Leu Asp 105 Ile	10 His Gln Arg Glu Thr 90 Gln His	Ser Ser Tyr Asp 75 Gly Lys Glu Leu	Leu Gly Asp 60 Val Asn Glu Asp	Arg Phe 45 Arg Leu Gly Gly Asn 125 Leu	Tyr 30 Leu Gln Gly Lys Leu 110 Ser	15 Asn Ala Lys Asn Asp 95 His Thr	Leu Glu Cys Lys 80 Leu Ser Arg Asn	
222 <400> 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala 65 Thr Trp Arg Met Leu Gln Ser Ser 130 Val Glu	E: 2 Leu Pro Leu 35 Leu Lys Asp Thr Glu 115 Gln	Gly 20 Ser Asp Pro Arg Leu 100 Ile	Pro 5 Ala Trp Gly Gln Glu 85 Ala Arg	Val Ala Asp Gln Gly 70 Thr His Val Tyr	Ala Gly Pro 55 Gln Arg Ile Cys Tyr 135	Glu Ser 40 Phe Trp Asp Lys Glu 120 Asp	Pro 25 Val Leu Ala Leu Asp 105 Ile	10 His Gln Arg Glu Thr 90 Gln His	Ser Ser Tyr Asp 75 Gly Lys Glu Leu Ser	Leu Gly Asp 60 Val Asn Glu Asp	Arg Phe 45 Arg Leu Gly Gly Asn 125 Leu	Tyr 30 Leu Gln Gly Lys Leu 110 Ser	15 Asn Ala Lys Asn Asp 95 His Thr	Leu Glu Cys Lys 80 Leu Ser Arg Asn	
222 <400> 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala 65 Thr Trp Arg Met Leu Gln Ser Ser 130 Val Glu 145	E: 2 Leu Pro Leu 35 Leu Lys Asp Thr Glu 115 Gln Thr	Gly 20 Ser Asp Pro Arg Leu 100 Ile His Glu	Pro 5 Ala Trp Gly Gln Glu 85 Ala Arg Phe Glu	Val Ala Asp Gln Gly 70 Thr His Val Tyr Trp 150	Ala Gly Pro 55 Gln Arg Ile Cys Tyr 135 Thr	Glu Ser 40 Phe Trp Asp Lys Glu 120 Asp Val	Pro 25 Val Leu Ala Leu Asp 105 Ile Gly Pro	10 His Gln Arg Glu Thr 90 Gln His Glu	Ser Ser Tyr Asp 75 Gly Lys Glu Leu Ser 155	Leu Gly Asp 60 Val Asn Glu Asp Phe 140 Ser	Arg Phe 45 Arg Leu Gly Gly Asn 125 Leu Arg	Tyr 30 Leu Gln Gly Lys Leu 110 Ser Ser	15 Asn Ala Lys Asn Asp 95 His Thr Gln	Leu Glu Cys Lys 80 Leu Ser Arg Asn Thr 160	
222 <400> 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala 65 Thr Trp Arg Met Leu Gln Ser Ser 130 Val Glu	E: 2 Leu Pro Leu 35 Leu Lys Asp Thr Glu 115 Gln Thr	Gly 20 Ser Asp Pro Arg Leu 100 Ile His Glu	Pro 5 Ala Trp Gly Gln Glu 85 Ala Arg Phe Glu Val	Val Ala Asp Gln Gly 70 Thr His Val Tyr Trp 150	Ala Gly Pro 55 Gln Arg Ile Cys Tyr 135 Thr	Glu Ser 40 Phe Trp Asp Lys Glu 120 Asp Val	Pro 25 Val Leu Ala Leu Asp 105 Ile Gly Pro	10 His Gln Arg Glu Thr 90 Gln His Glu Gln Lys	Ser Ser Tyr Asp 75 Gly Lys Glu Leu Ser 155	Leu Gly Asp 60 Val Asn Glu Asp Phe 140 Ser	Arg Phe 45 Arg Leu Gly Gly Asn 125 Leu Arg	Tyr 30 Leu Gln Gly Lys Leu 110 Ser Ser	15 Asn Ala Lys Asn Asp 95 His Thr Gln Gln Lys	Leu Glu Cys Lys 80 Leu Ser Arg Asn Thr 160	
222 <400> 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242	Met Gly 1 Ala Pro Thr Val Val His 50 Arg Ala 65 Thr Trp Arg Met Leu Gln Ser Ser 130 Val Glu 145	E: 2 Leu Pro Leu 35 Leu Lys Asp Thr Glu 115 Gln Thr Met	Gly 20 Ser Asp Pro Arg Leu 100 Ile His Glu Asn	Pro 5 Ala Trp Gly Gln Glu 85 Ala Arg Phe Glu Val 165	Val Ala Asp Gln Gly 70 Thr His Val Tyr Trp 150 Arg	Ala Gly Pro 55 Gln Arg Ile Cys Tyr 135 Thr	Glu Ser 40 Phe Trp Asp Lys Glu 120 Asp Val Phe	Pro 25 Val Leu Ala Leu Asp 105 Ile Gly Pro Leu	10 His Gln Arg Glu Thr 90 Gln His Glu Gln Lys 170	Ser Ser Tyr Asp 75 Gly Lys Glu Leu Ser 155 Glu	Leu Gly Asp 60 Val Asn Glu Asp Phe 140 Ser Asp	Arg Phe 45 Arg Leu Gly Gly Asn 125 Leu Arg	Tyr 30 Leu Gln Gly Lys Leu 110 Ser Ser Ala Met	15 Asn Ala Lys Asn Asp 95 His Thr Gln Gln Lys 175	Leu Glu Cys Lys 80 Leu Ser Arg Asn Thr 160 Thr	

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/855,612A

DATE: 12/04/2001

TIME: 17:55:20